

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:30:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251078.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10251078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:30:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,979,674
Mapped reads	3,814,151 / 95.84%
Unmapped reads	165,523 / 4.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,382 / 0.84%
Read min/max/mean length	30 / 80 / 80.3
Duplicated reads (estimated)	639,191 / 16.06%
Duplication rate	14.45%
Clipped reads	583,013 / 14.65%

2.2. ACGT Content

Number/percentage of A's	86,509,759 / 29.34%
Number/percentage of C's	58,746,695 / 19.93%
Number/percentage of T's	87,347,856 / 29.63%
Number/percentage of G's	62,219,766 / 21.1%
Number/percentage of N's	2,817 / 0%
GC Percentage	41.03%

2.3. Coverage

Mean	0.0953

Standard Deviation	1.0293
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	47.91
----------------------	-------

2.5. Mismatches and indels

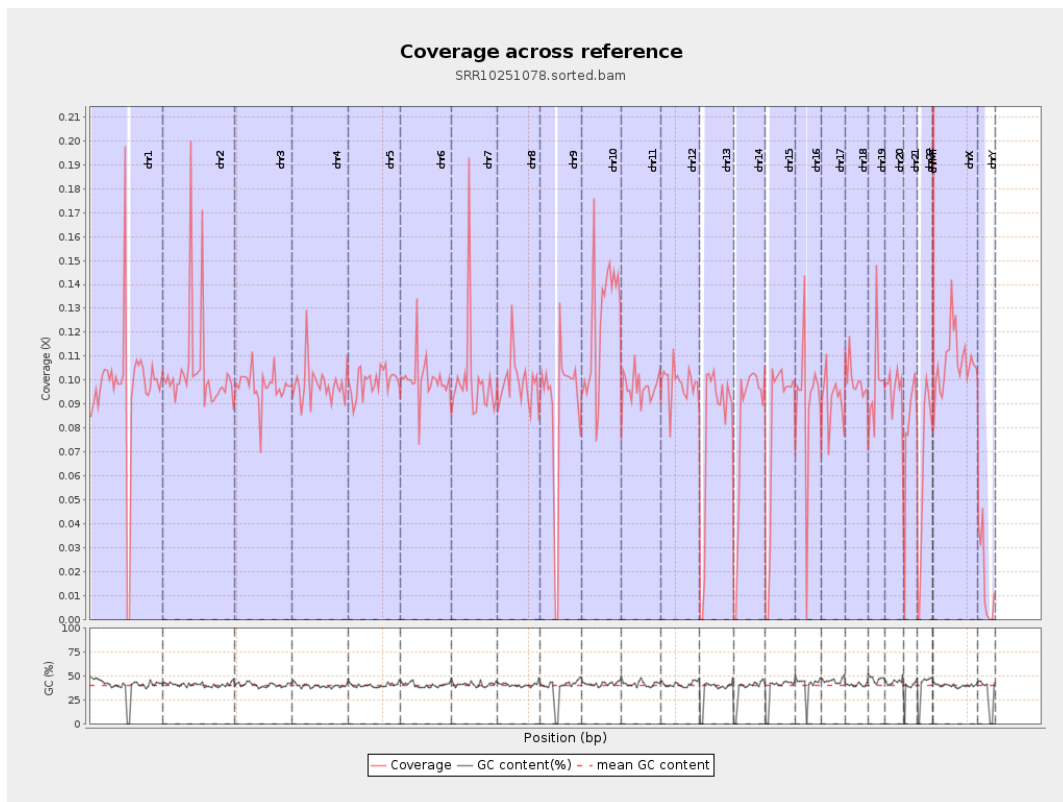
General error rate	0.64%
Mismatches	1,818,569
Insertions	36,729
Mapped reads with at least one insertion	0.95%
Deletions	112,566
Mapped reads with at least one deletion	2.9%
Homopolymer indels	44.59%

2.6. Chromosome stats

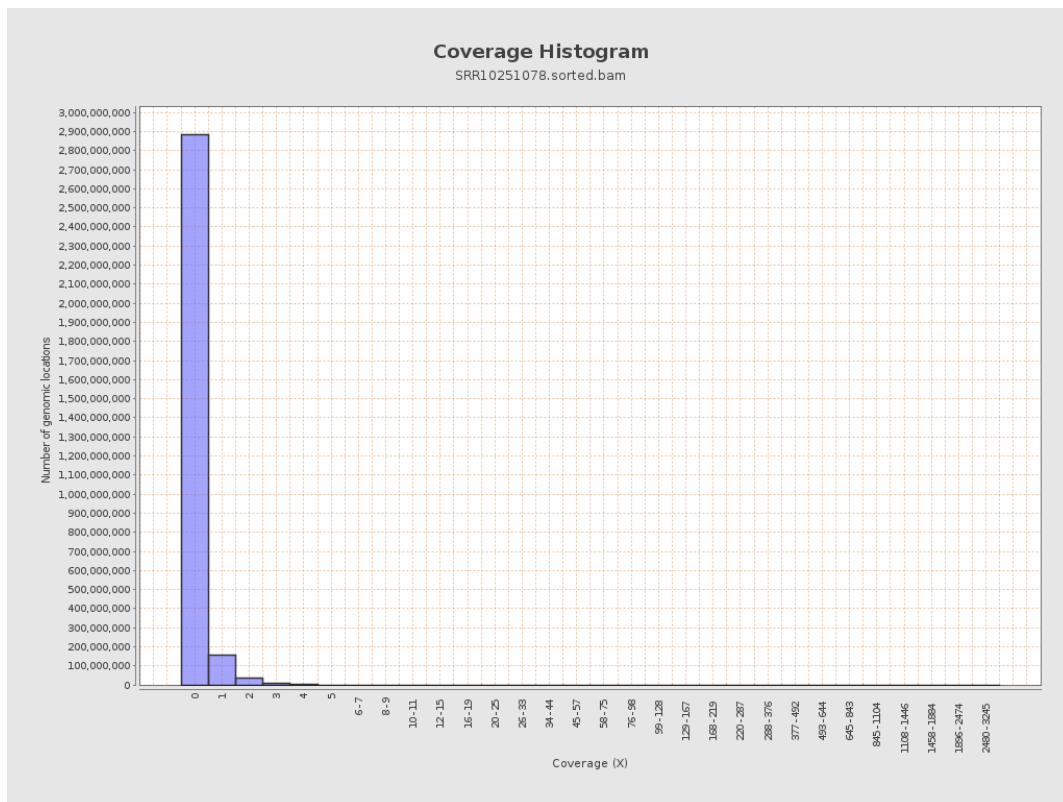
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24002734	0.0963	2.1913
chr2	243199373	25253747	0.1038	1.2765
chr3	198022430	19300720	0.0975	0.4113
chr4	191154276	18866980	0.0987	0.4914
chr5	180915260	17965263	0.0993	0.4322
chr6	171115067	17166641	0.1003	0.6048
chr7	159138663	15871573	0.0997	1.6124

chr8	146364022	14442336	0.0987	0.6916
chr9	141213431	12584163	0.0891	1.1922
chr10	135534747	16690353	0.1231	1.0275
chr11	135006516	13089304	0.097	0.6285
chr12	133851895	13236846	0.0989	0.4332
chr13	115169878	9155698	0.0795	0.3626
chr14	107349540	8811050	0.0821	0.6297
chr15	102531392	8258792	0.0805	0.3679
chr16	90354753	8115489	0.0898	0.79
chr17	81195210	7531956	0.0928	0.533
chr18	78077248	7828343	0.1003	1.2666
chr19	59128983	5848540	0.0989	1.8745
chr20	63025520	6065977	0.0962	0.4623
chr21	48129895	3863141	0.0803	0.4313
chr22	51304566	3276116	0.0639	0.3643
chrMT	16571	144068	8.694	5.6726
chrX	155270560	16710775	0.1076	0.5305
chrY	59373566	947269	0.016	0.8729

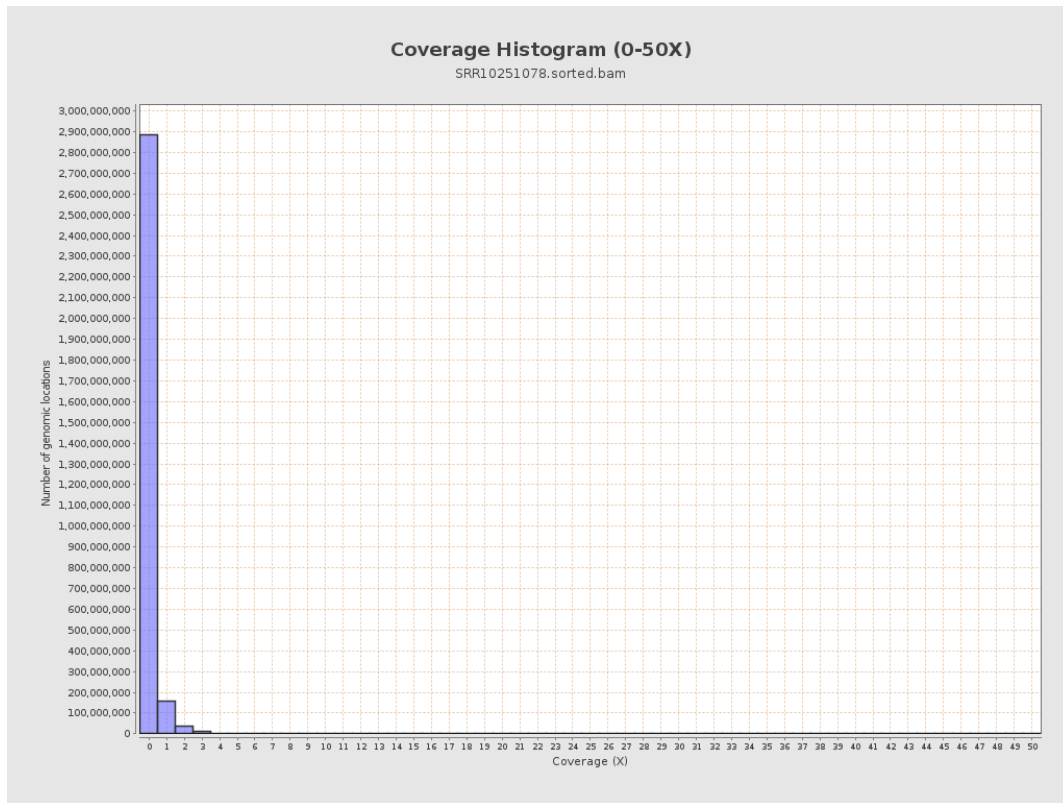
3. Results : Coverage across reference



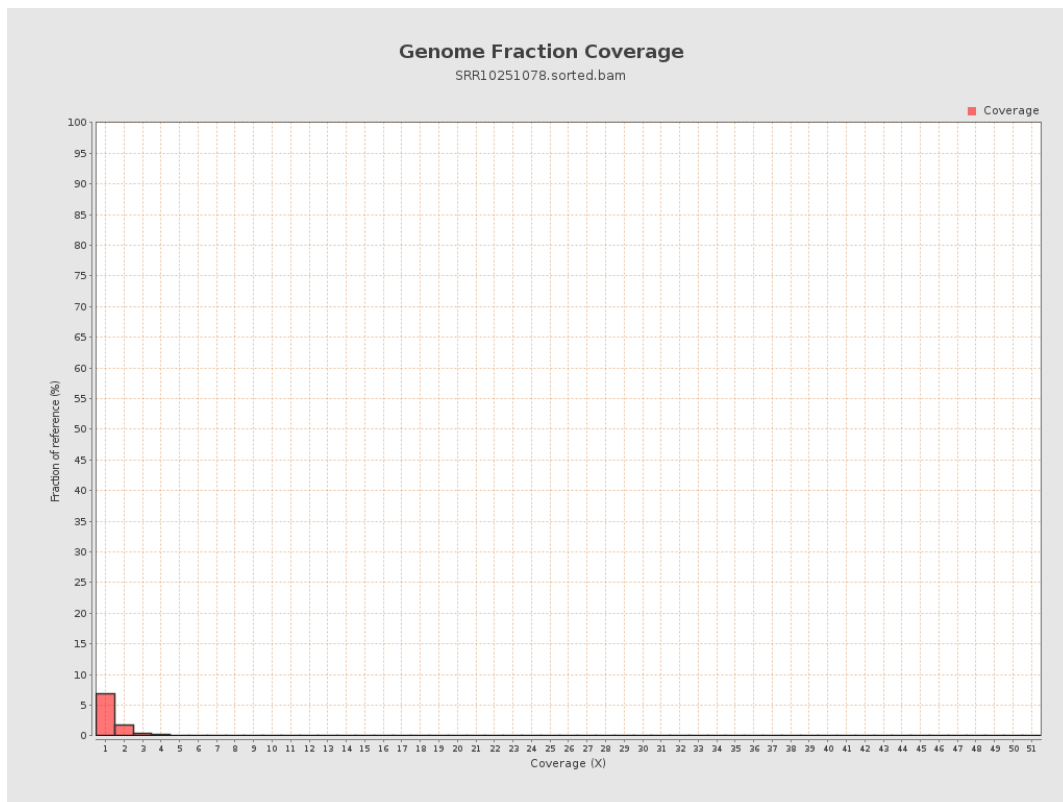
4. Results : Coverage Histogram



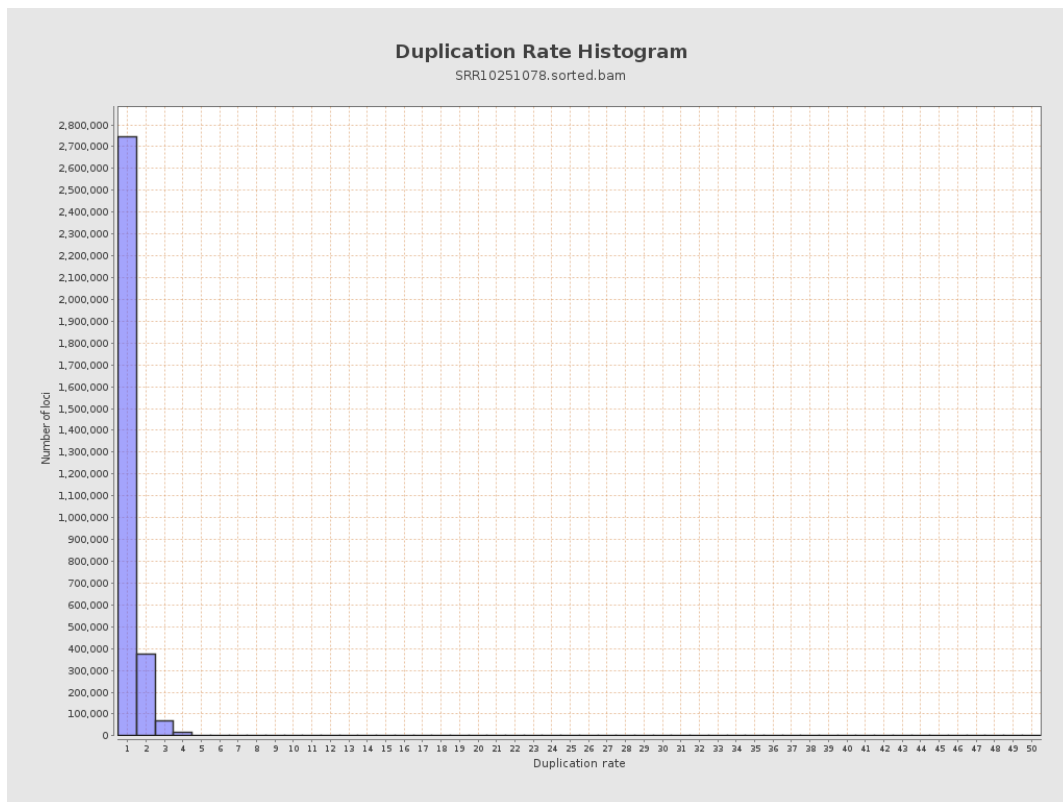
5. Results : Coverage Histogram (0-50X)



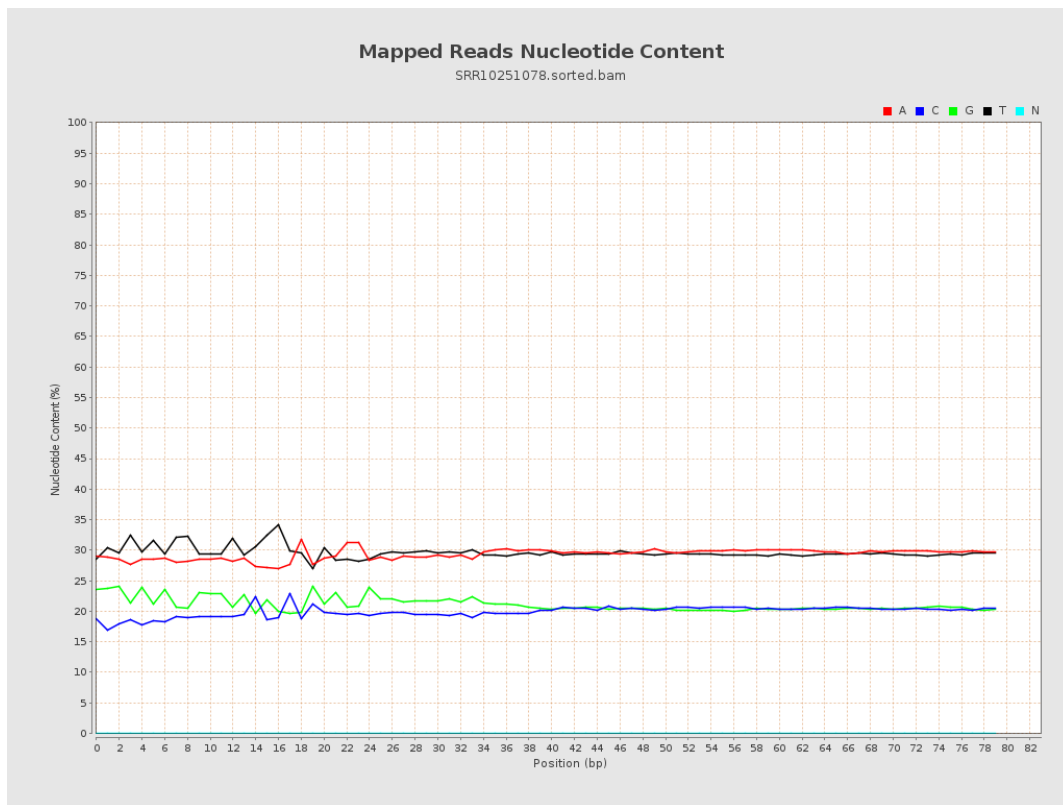
6. Results : Genome Fraction Coverage



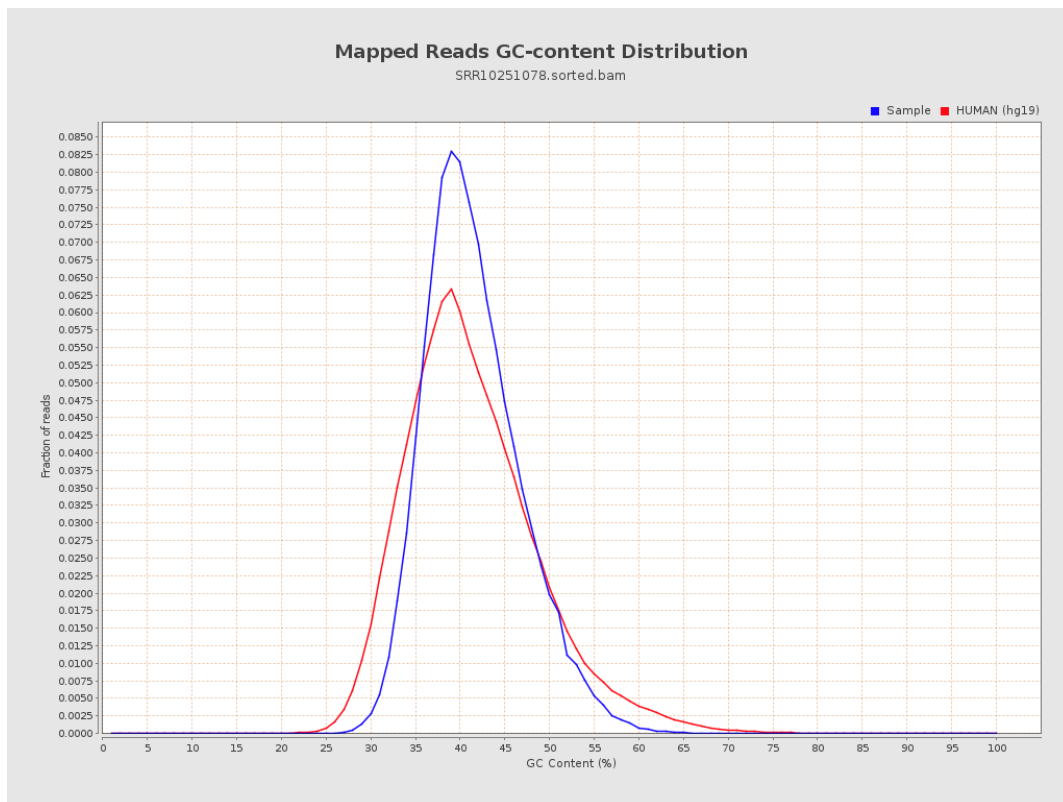
7. Results : Duplication Rate Histogram



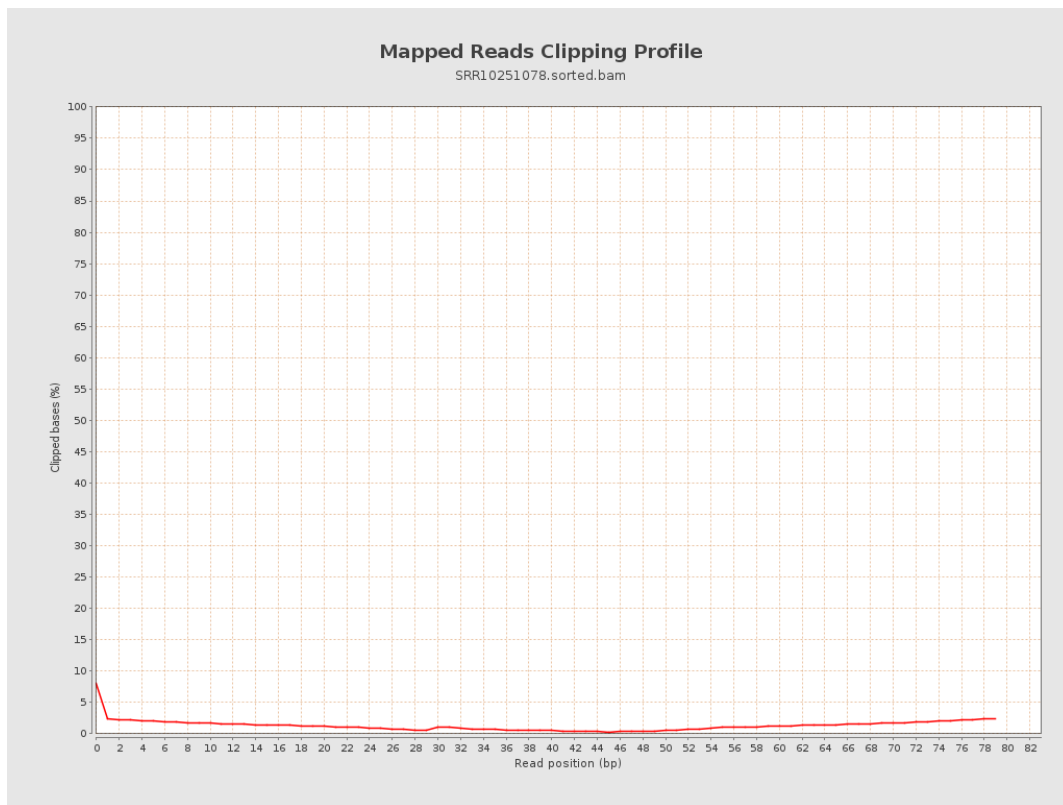
8. Results : Mapped Reads Nucleotide Content



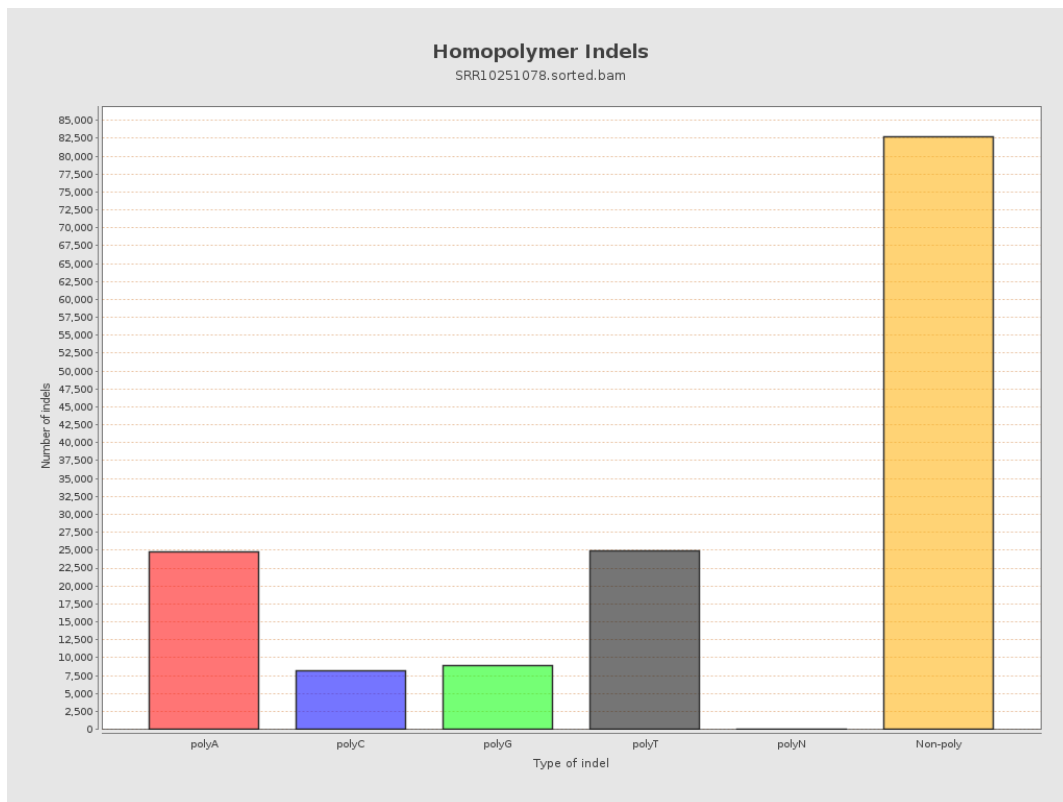
9. Results : Mapped Reads GC-content Distribution



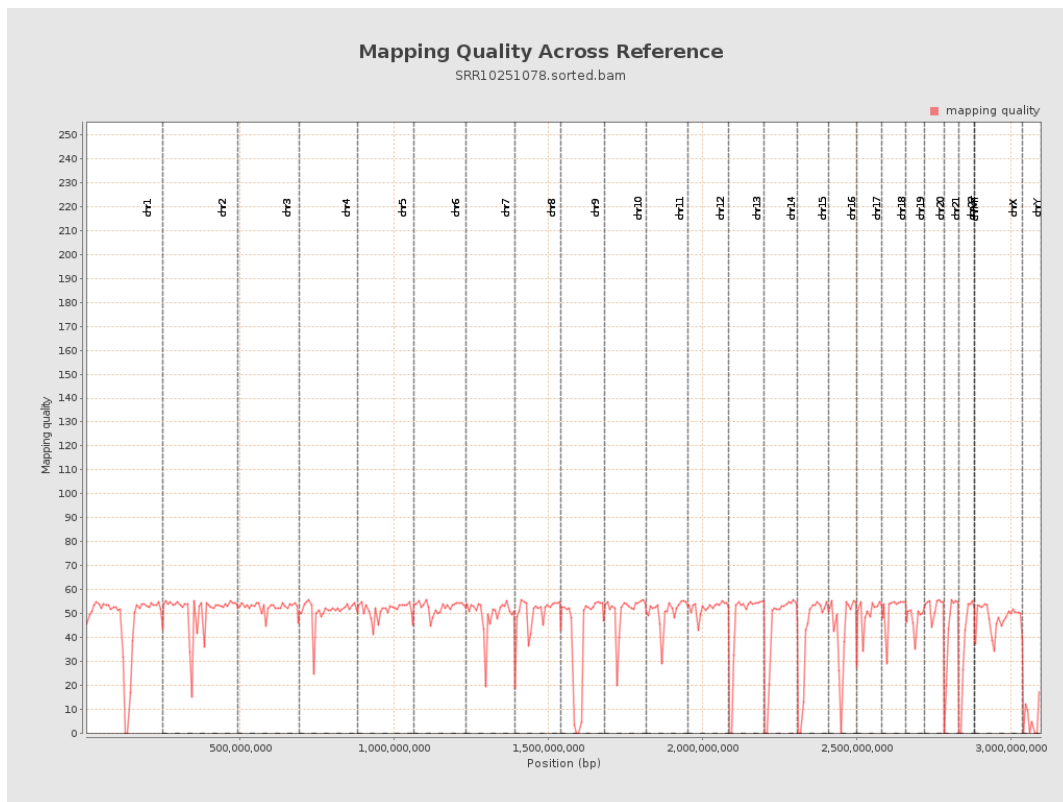
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

